

SEQUENCE LISTING

<110> Rayapati, P. John
Crafton, Corey M.

<120> Nucleotide Sequences for Transcriptional Regulation in
Corynebacterium glutamicum

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<151> 2000-11-15

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<170> PatentIn version 3.0

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<213> Corynebacterium glutamicum

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<213> Corynebacterium glutamicum

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<213> *Corynebacterium glutamicum*

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<213> *Corynebacterium glutamicum*

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<213> Corynebacterium glutamicum

<213> Corynebacterium glutamicum

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<211> 500

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205 210 215

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aat	gtt	ccg	gcg	tta	ttt	ctt	gat	gtc	tct	gac	cag	aca	ccc	atc	aac	480		
Asn	Val	Pro	Ala	Leu	Phe	Leu	Asp	Val	Ser	Asp	Gln	Thr	Pro	Ile	Asn			
			145				150				155				160			
agt	att	att	ttc	tcc	cat	gaa	gac	ggt	acg	cga	ctg	ggc	gtg	gag	cat	528		
Ser	Ile	Ile	Phe	Ser	His	Glu	Asp	Gly	Thr	Arg	Leu	Gly	Val	Glu	His			
			165				170				175							
ctg	gtc	gca	ttg	ggt	cac	cag	caa	atc	gcg	ctg	tta	gcg	ggc	cca	tta	576		
Leu	Val	Ala	Leu	Gly	His	Gln	Gln	Ile	Ala	Leu	Leu	Ala	Gly	Pro	Leu			
			180				185				190							
agt	tct	gtc	tcg	gcg	cgt	ctg	cgt	ctg	gct	ggc	tgg	cat	aaa	tat	ctc	624		
Ser	Ser	Val	Ser	Ala	Arg	Leu	Arg	Leu	Ala	Gly	Trp	His	Lys	Tyr	Leu			
			195				200				205							
act	cgc	aat	caa	att	cag	ccg	ata	gcg	gaa	cgg	gaa	ggc	gac	tgg	agt	672		
Thr	Arg	Asn	Gln	Ile	Gln	Pro	Ile	Ala	Glu	Arg	Glu	Gly	Asp	Trp	Ser			
			210				215				220							
gcc	atg	tcc	ggt	ttt	caa	caa	acc	atg	caa	atg	ctg	aat	gag	ggc	atc	720		
Ala	Met	Ser	Gly	Phe	Gln	Gln	Thr	Met	Gln	Met	Leu	Asn	Glu	Gly	Ile			
			225				230				235				240			
gtt	ccc	act	gcg	atg	ctg	gtt	gcc	aac	gat	cag	atg	gcg	ctg	ggc	gca	768		
Val	Pro	Thr	Ala	Met	Leu													

gta gtg gga tac gac gat acc gaa gac agc tca tgt tat atc ccg ccg 864
Val Val Gly Tyr Asp Asp Thr Glu Asp Ser Ser Cys Tyr Ile Pro Pro
275 280 285

tca acc acc atc aaa cag gat ttt cgc ctg ctg ggg caa acc agc gtg 912
Ser Thr Thr Ile Lys Gln Asp Phe Arg Leu Leu Gly Gln Thr Ser Val
290 295 300

gac cgc ttg ctg caa ctc tct cag ggc cag gcg gtg aag ggc aat cag 960
Asp Arg Leu Leu Gln Leu Ser Gln Gly Gln Ala Val Lys Gly Asn Gln
305 310 315 320

ctg ttg ccc gtc tca ctg gtg aaa aga aaa acc acc ctg gcg ccc aat 1008
Leu Leu Pro Val Ser Leu Val Lys Arg Lys Thr Thr Leu Ala Pro Asn
325 330 335

acg caa acc gcc tct ccc cgc gcg ttg gcc gat tca tta atg cag ctg 1056
Thr Gln Thr Ala Ser Pro Arg Ala Leu Ala Asp Ser Leu Met Gln Leu
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Ala Arg Gln Val Ser Arg Leu Glu Ser Gly Gln
355 360

<210> 29

<211> 363

<212> PRT

<213> Escherichia coli

<400> 29

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Gly Val Ser Tyr Gln Thr Val Ser Arg Val Val Asn Gln Ala Ser His
20 25 30

Val Ser Ala Lys Thr Arg Glu Lys Val Glu Ala Ala Met Ala Glu Leu
35 40 45

Asn Tyr Ile Pro Asn Arg Val Ala Gln Gln Leu Ala Gly Lys Gln Ser
50 55 60

Leu Leu Ile Gly Val Ala Thr Ser Ser Leu Ala Leu His Ala Pro Ser
65 70 75 80

Gln Ile Val Ala Ala Ile Lys Ser Arg Ala Asp Gln Leu Gly Ala Ser
85 90 95

Val Val Val Ser Met Val Glu Arg Ser Gly Val Glu Ala Cys Lys Ala

1056-1092

			100					105					110		
Ala	Val	His	Asn	Leu	Leu	Ala	Gln	Arg	Val	Ser	Gly	Leu	Ile	Ile	Asn
		115					120					125			
Tyr	Pro	Leu	Asp	Asp	Gln	Asp	Ala	Ile	Ala	Val	Glu	Ala	Ala	Cys	Thr
	130					135					140				
Asn	Val	Pro	Ala	Leu	Phe	Leu	Asp	Val	Ser	Asp	Gln	Thr	Pro	Ile	Asn
145					150					155					160
Ser	Ile	Ile	Phe	Ser	His	Glu	Asp	Gly	Thr	Arg	Leu	Gly	Val	Glu	His
				165					170					175	
Leu	Val	Ala	Leu	Gly	His	Gln	Gln	Ile	Ala	Leu	Leu	Ala	Gly	Pro	Leu
			180					185					190		
Ser	Ser	Val	Ser	Ala	Arg	Leu	Arg	Leu	Ala	Gly	Trp	His	Lys	Tyr	Leu
		195					200					205			
Thr	Arg	Asn	Gln	Ile	Gln	Pro	Ile	Ala	Glu	Arg	Glu	Gly	Asp	Trp	Ser
	210					215					220				
Ala	Met	Ser	Gly	Phe	Gln	Gln	Thr	Met	Gln	Met	Leu	Asn	Glu	Gly	Ile
225					230					235					240
Val	Pro	Thr	Ala	Met	Leu	Val	Ala	Asn	Asp	Gln	Met	Ala	Leu	Gly	Ala
				245					250					255	
Met	Arg	Ala	Ile	Thr	Glu	Ser	Gly	Leu	Arg	Val	Gly	Ala	Asp	Ile	Ser
			260					265					270		
Val	Val	Gly	Tyr	Asp	Asp	Thr	Glu	Asp	Ser	Ser	Cys	Tyr	Ile	Pro	Pro
		275					280					285			
Ser	Thr	Thr	Ile	Lys	Gln	Asp	Phe	Arg	Leu	Leu	Gly	Gln	Thr	Ser	Val
	290					295					300				
Asp	Arg	Leu	Leu	Gln	Leu	Ser	Gln	Gly	Gln	Ala	Val	Lys	Gly	Asn	Gln
305					310					315					320
Leu	Leu	Pro	Val	Ser	Leu	Val	Lys	Arg	Lys	Thr	Thr	Leu	Ala	Pro	Asn
				325					330					335	
Thr	Gln	Thr	Ala	Ser	Pro	Arg	Ala	Leu	Ala	Asp	Ser	Leu	Met	Gln	Leu
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Ala Arg Gln Val Ser Arg Leu Glu Ser Gly Gln
355 360

<210> 30

<211> 1511

<212> DNA

<213> Escherichia coli

<400> 30

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cagagtatgc cgggtgtctct tatcagaccg tttcccgctt ggtgaaccag gccagccacg	180
tttctgcgaa aacgcgggaa aaagtggaa ggcgatggc ggagctgaat tacattccca	240
accgcgtggc acaacaactg gcgggcaaac agtcgttget gattggcgtt gccacctcca	300
gtctggccct gcaogcgccg tcgcaaattg tcgcggcgat taaatctcgc gccgatcaac	360
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090976-1501

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<210>	33
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		cgccttcagt	ttgggctact	tggttctggg	cgaaaaattc	caagtcgtgg	actgggaatg	180
		gatcgccatg	ggcatcgac	tcttggtgat	gattgtttcc	accattgcac	tgtctcgtac	240
		aagcacaatg	cgcgcggat	cgaaaaggta	aaactocaaa	gttccccccc	cgagacatga	300

cagcactgga actgggcgtc gaaaagcttt tttaaaagaa aactcccccc gagttgctac 360
ccacaccaca aagttgttgt atgcttcacc acatgaattc gcgtgcgaat ctacttcttc 420
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<210> 34

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<212> DNA

<213> Corynebacterium glutamicum

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tcgccactgc tgagcattga gctgccttca gagctgcctg gccaggtttc gtttccatcg 180
actggttttc catcatcatc aaggatctgt gatgagggtga tgttgctctga gagctgtgtc 240
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gctgtaacaa ggggtcaaagt acttcgacgc aaagacaaaa cttttctcct ggcaataaat 360
atgcggatatt actatggaaa caagatagaa gattggatag cgaaagctat cctcaactcg 420
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<211> 500

<212> DNA

<213> Corynebacterium glutamicum

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ttgtgagaat cctgattcct taaccgaagt gggggagttt tgggggtggg aattttcgtg 180
cgttgaggaa ttggaaactc gatgtgtgta gcatgacaca ccatgaccat tattcgactt 240
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099743-1501

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